

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 17, 2004, 21:02:23 ; Search time 13.0543 Seconds

(without alignments)
4951.677 Million cell updates/sec

Title: US-08-628-829-2

Perfect score: 3467
Sequence: 1 MTTAVPAVPSKLVMTMLNAGS.....PQDRPPRELKHVPRITW 672

ing table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3467	100.0	687	2	A46212
2	3188.5	92.0	1493	2	T10757
3	586.5	16.9	651	2	A96591
4	586.5	16.9	706	2	A48084
5	574.5	16.6	1478	2	S20117
6	568	16.4	659	1	A39723
7	536	15.5	883	2	A96662
8	528.5	15.2	738	1	S51380
9	525	15.1	1338	2	T30565
10	519.5	15.0	608	2	G96575
11	499.5	14.4	1116	2	T38073
12	479	13.8	652	2	H86221
13	472.5	13.6	582	2	T51625
14	462	13.3	608	2	T01833
15	460.5	13.3	1607	2	T03022
16	448.5	12.9	650	2	JC4673
17	441	12.7	372	2	T52621
18	441	12.7	535	2	T51736
19	436	12.6	560	2	D85084
20	435.5	12.6	1401	2	T39225
21	427	12.3	572	2	T01836
22	424.5	12.2	1379	2	JC5778
23	424	12.2	1579	2	S59801
24	423	12.2	773	2	T01835
25	422	12.2	560	2	T14616
26	420	12.1	372	2	T02550
27	416	12.0	836	2	B96716
28	411	11.9	1387	2	T16511
29	408.5	11.8	1288	2	JE0363

30	404.5	11.7	1895	2	T06609	disease resistance
31	395	11.4	471	2	T39232	probable serine th
32	392	11.3	658	2	T39500	serine/threonine-s
33	392	11.3	756	2	T50298	MAP kinase kinase
34	384	11.1	403	2	JC5974	autora-related kin
35	383.5	11.1	525	2	S58682	serine/threonine-s
36	378	10.9	544	2	S40482	serine/threonine-s
37	377.5	10.9	339	2	C86185	hypothetical prote
38	375.5	10.8	544	2	A57597	beta-p21-activated
39	375.5	10.8	545	2	G01773	p21-activated prot
40	374.5	10.8	1230	2	T18256	probable serine/th
41	374.5	10.8	1230	2	T18259	serine/threonine p
42	374	10.8	650	2	P0170	protein kinase Pak
43	373	10.8	1418	2	T15232	hypothetical prote
44	372.5	10.7	939	2	S28394	probable serine/th
45	370.5	10.7	1062	2	S46367	protein kinase CDC

ALIGNMENTS

RESULT 1	
A46212	
MEK kinase - mouse	
C:Species: Mus musculus (house mouse)	
C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-May-1999	
C/Accession: A46212	
R/Lange-Carter, C.A.; Pleiman, C.M.; Gardner, A.M.; Blumer, K.J.; Johnson, G.L.	
Science 260, 315-319, 1993	
A>Title: A divergence in the MAP kinase regulatory network defined by MEK kinase and Raf.	
A/Reference number: A46212; PMID:93227040; PMID:8385802	
A/Accession: A46212	
A>Status: preliminary; not compared with conceptual translation	
A/Molecule type: nucleic acid	
A/Residues: 1-687 <LAN>	
A/Experimental source: brain	
A/Note: sequence extracted from NCBI backbone (NCBI:129292)	
C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog	
C/Keywords: ATP	
F:416-683/Domain: protein kinase homology <KIN>	
F:424-432/Region: protein kinase ATP-binding motif	
Query Match	100.0%; Score 3467; DB 2; Length 687;
Best Local Similarity	Pred. No. 1.3e-133; Indels 0; Gaps 0;
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MTTAVPAVPSKLVMTMLNAGSSTHTFTMRRLMAIADEVEIAEVIQUGVEDTVGHDSDIQ 60
DB	16 MTTAVPAVPSKLVMTMLNAGSSTHTFTMRRLMAIADEVEIAEVIQUGVEDTVGHDSDIQ 75
QY	61 AAAPTSCLENSLEHTVHEKTKGKLSATRLGASSSDIDRLAGVSGIPSSITTEQPKP 120
DB	76 AAAPTSCLENSLEHTVHEKTKGKLSATRLGASSSDIDRLAGVSGIPSSITTEQPKP 135
QY	121 AVOTKRPHSOCLNSSLPLSHAOIMFPAPSPASASVSDISKHQAQVPCIKIPASPO 180
DB	136 AVOTKRPHSOCLNSSLPLSHAOIMFPAPSPASASVSDISKHQAQVPCIKIPASPO 195
QY	181 TORKFSLOFORNCSEHRSDQLSPVFTQSRPPSSNIHRPKSPRPVPGSTSKLGATKSS 240
DB	196 TORKFSLOFORNCSEHRSDQLSPVFTQSRPPSSNIHRPKSPRPVPGSTSKLGATKSS 255
QY	241 MTLIDGASRCDDSPGGGNSGNNAVIPSDETVFTPEDEKCRDLVNTLNSIEDLLIABSM 300
DB	256 MTLIDGASRCDDSPGGGNSGNNAVIPSDETVFTPEDEKCRDLVNTLNSIEDLLIABSM 315
QY	301 PSSDTTFVFKSEAVVSPKAEKNDPTVKDVVHNQCKKMEAEEREALAIAMASASOD 360
DB	316 PSSDTTFVFKSEAVVSPKAEKNDPTVKDVVHNQCKKMEAEEREALAIAMASASOD 375
QY	361 ALPIVPOQVENGEDIIIIQODTPETLPHTAKAKOPYREDAEWLKGQOIGLGFSSCYOA 420
DB	376 ALPIVPOQVENGEDIIIIQODTPETLPHTAKAKOPYREDAEWLKGQOIGLGFSSCYOA 435

QY 421 QDVGTGLMAVKQVYVYRNTSSQEEVEALREIRRMGHNLNPNIIIRMLGATCEKSNYN 480
 DB 436 QDVGTGLMAVKQVYVYRNTSSQEEVEALREIRRMGHNLNPNIIIRMLGATCEKSNYN 495
 QY 481 LFIEMWAGSVVALLSKYGAFKESVYVNTYEQILRGSLYHENOIIHRDVKGANLLIDST 540
 DB 496 LFIEMWAGSVVALLSKYGAFKESVYVNTYEQILRGSLYHENOIIHRDVKGANLLIDST 555
 QY 541 GQRLRIADFGAARLASKGTGAGEFQGLLGTIAFMAPEVLRGQYGRSCDWSVGCAT 600
 DB 556 GQRLRIADFGAARLASKGTGAGEFQGLLGTIAFMAPEVLRGQYGRSCDWSVGCAT 615
 QY 601 EVACAKPMMNAEKSHNLALIFKIASATTAAPSIPSHLSPGLRDVAVRCLTELQPODRPSPR 660
 DB 616 EVACAKPMMNAEKSHNLALIFKIASATTAAPSIPSHLSPGLRDVAVRCLTELQPODRPSPR 675
 QY 661 ELKHVPFRTTW 672
 DB 676 ELKHVPFRTTW 687

RESULT 2

Species: Rattus norvegicus (Norway rat)
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C/Accession: T10757
 R.Xu, S.; Robbins, D.J.; Christerson, L.B.; English, J.M.; Vanderbilt, C.A.; Cobb, M.H.
 Proc. Natl. Acad. Sci. U.S.A. 93, 5291-5295, 1996
 A/Title: Cloning of rat MEK kinase 1 cDNA reveals an endogenous membrane-associated 195-
 A/Reference number: Z17123; MUID:96224276; PMID:8643568
 A/Accession: T10757
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1493 <XUS>
 A/Cross-References: EMBL:U48596; NID:g1354136; PIDN:AAC52596.1; PID:g1354137
 C/Genetics:
 A/Gene: MEK1
 C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C/Keywords: ATP; phosphotransferase; protein kinase

Query Match 92.0%; Score 3188.5; DB 2; Length 1493;
 Best Local Similarity 91.9%; Pred. No. 5, 2e-122;
 Matches 622; Conservative 18; Mismatches 32; Indels 5; Gaps 1;
 QY 1 MTAAPAVSKVYTMNANSGSTHTFMRRLMAIADEVEIAYIOGVEDYVGHDSIQ 60
 DB 817 MVTVPPLPSKLVMTLSAGSSHFARMRLMAIADEVEIAYIOGVEDYVGHDSIQ 876
 QY 61 AAVPTSCLENSLIEHTVREKTKGSLATRLSASSEDISDRLAGVGVGLPSTTTQOPRP 120
 DB 877 ALAPRPYPPSSSLIEHTVREKTKGSLATRLSASSEDISDRLAGVGVGLPSTTTQOPRP 936
 QY 121 AVOTKRPHSQCLNSPLSHAOIMPPAPAPCGSABSV-----DISKRPOAFVBCIKP 175
 DB 937 TVOTKRPHSQCLNSPLSPOLMPAPISAPCSASVPAGSVTDASKRPRAFVCIKP 996
 QY 176 SASPQORFSLQFONCEHNDSDLSVFTOSRPPSSNTHRPSPRPVPGSTSKLD 235
 DB 997 SASPQORFSLQFONCEHNDSDLSVFTOSRPPSSNTHRAASRPVPSTSKLD 1056
 QY 236 ATKSWTLTLGASRCDPSFGGGGNGNAVIPSEDEVTFTVEDKGLDVNTELENSIEDL 295
 DB 1057 ASKNSWTLTLGASRCDPSFGGGGNGNAVIPSEDEVTFTVEDKGLDVNTELENSIEDL 1116
 QY 296 LEASMPSSDTTYTFKSEVAVLSPEKAEVDYKDVNHNQCKEKEAESEELATAMAM 355
 DB 1117 LEASMPSSDTTYTFKSEVAVLSPEKAEVDYKDVNHNQCKEKEAESEELATAMAM 1176
 QY 356 SASDOLPIVPOLOVENGDIIIIIODTTETTLPGHTKAKQPIREDAEMLKGOIGGAPS 415
 DB 1177 SASDOLPIVPOLOVENGDIIIIIODTTETTLPGHTKANEPYREDTEMLKGOIGGAPS 1236

QY 416 SCYQADVGITGLMAVKQVYVYRNTSSQEEVEALREIRRMGHNLNPNIIIRMLGATCE 475
 DB 1237 SCYQADVGITGLMAVKQVYVYRNTSSQEEVEALREIRRMGHNLNPNIIIRMLGATCE 1296
 QY 476 KSNYMLFIEMWAGSVVALLSKYGAFKESVYVNTYEQILRGSLYHENOIIHRDVKGANL 535
 DB 1297 KSNYMLFIEMWAGSVVALLSKYGAFKESVYVNTYEQILRGSLYHENOIIHRDVKGANL 1356
 QY 536 LIDSTGQRLRIADFGAARLASKGTGAGEFQGLLGTIAFMAPEVLRGQYGRSCDWSV 595
 DB 1357 LIDSTGQRLRIADFGAARLASKGTGAGEFQGLLGTIAFMAPEVLRGQYGRSCDWSV 1416
 QY 596 GCALIEMACAKPMMNAEKSHNLALIFKIASATTAAPSIPSHLSPGLRDVAVRCLTELQPOD 655
 DB 1417 GCALIEMACAKPMMNAEKSHNLALIFKIASATTAAPSIPSHLSPGLRDVAVRCLTELQPOD 1476
 QY 656 RPPSRELKHVPFRTTW 672
 DB 1477 RPPSRELKHVPFRTTW 1493

RESULT 3

Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
 C/Accession: A96591
 R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chiu, C.M.; Chung, M.K.; Com, U.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Hultzar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A66141; MUID:21016719; PMID:11130712
 A/Accession: A96591
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-651 <STO>
 A/Cross-References: GB:AE005173; NID:99857521; PIDN:AAG00876.1; GSPDB:GN00141
 A/Gene: T24C10.7
 C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 16.9%; Score 586.5; DB 2; Length 651;
 Best Local Similarity 42.9%; Pred. No. 4, 1e-17;
 Matches 118; Conservative 56; Mismatches 90; Indels 11; Gaps 5;
 QY 394 KQYREDDEMLKGOIGLGAPESSCYQADVGITGLMAVKQVYVYRNTSSQEEVEAL 451
 DB 63 KQYREDDEMLKGOIGLGAPESSCYQADVGITGLMAVKQVYVYRNTSSQEEVEAL 451
 QY 452 REIRRMGHNLNPNIIIRMLGATCEKSNYNLFIEEMWAGSVVALLSKYGAFKESVYVNT 511
 DB 119 REIRRMGHNLNPNIIIRMLGATCEKSNYNLFIEEMWAGSVVALLSKYGAFKESVYVNT 511
 QY 512 QLLRGSLYHENOIIHRDVKGANLLIDSTGQRLRIADFGAARLASKGTGAGEFQGLL 571
 DB 179 QLLRGSLYHENOIIHRDVKGANLLIDSTGQRLRIADFGAARLASKGTGAGEFQGLL 571
 QY 572 TIAFMAPEVLRGQYGRSCDWSVGCALIEMACAKPMMNAEKSHNLALIFKIASATTA 631
 DB 236 TIAFMAPEVLRGQYGRSCDWSVGCALIEMACAKPMMNAEKSHNLALIFKIASATTA 631
 QY 632 SIPSHLSPGLRDVAVRCLTELQPODRPSPRELKHVP 666
 DB 294 SIPSHLSPGLRDVAVRCLTELQPODRPSPRELKHVP 666

RESULT 4
A46084
SPEL1 protein kinase homolog NPX1 - common tobacco
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 16-Feb-1994 #sequence_rev18-Nov-1994 #text_change 19-Dec-1997
C/Accession: A46084
R/Banno, H.; Hirano, K.; Nakamura, T.; Irie, K.; Nomoto, S.; Matsumoto, K.; Machida, Y.
Mol. Cell. Biol. 13, 4745-4752, 1993
A>Title: NPX1, a tobacco gene that encodes a protein with a domain homologous to yeast
A/Reference number: A46084; MUID:93350268; PMID:8336712
A/Accession: A46084
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-706 <BAN>
Experimental source: By-2 cells
Description: Sequence extracted from NCBI backbone (NCBIN:135697, NCBI:135698)
C/Keywords: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C/Keywords: ATP
F:94-358/Domain: protein kinase ATP-binding motif
F:102-110/Region: protein kinase ATP-binding motif

Query Match: 16.9%; Score 586.5; DB 2; Length 706;
Best Local Similarity 41.7%; Pred. No. 4,4e-17;
Matches 120; Conservative 60; Mismatches 95; Indels 13; Gaps 6;

QY 387 LGHTAKAP--YRED---AEWLKGOQIGLGFSSCYQADYGTGLMAVQYTVVNT 440
DB 74 LPSISKAELPAKARKDTPPIRRKKEGEMICGAFGVYGMVNDSEGLAIKEVSIAMNG 133
QY 441 SSEQ--EEVVEALREIRRMGHLNHNIRMLGATEKSNVNFIFIMAGGSVAHLISKY 498
DB 134 ASREBQAQVRELEEVNLKNSHPNRYVLTABAGSLNLFVFGGSISSLGKF 193
QY 499 GAFKESVINTYEQLLRGLSYLHENOQIHRDYKANLIDSTQRLRIADFGAARLASK 558
DB 194 GSPBESVIMRYTKQLLGLLEYLHKNGIMRDIGANILVDNKG-CIKLADFGASKVVEL 252
QY 559 GFGAGFQOGLGTIFMAPEVLARGQYGRSCVNSVGCALITMACAKPPMAEKSNHL 618
DB 253 ATMTG--AKSMKTPPMAPPEVLQGHSPSADIMVGVCTIEMAGKPPWS--QQYQEV 308
QY 619 ALIFKIASATAPISPSHSLPGLDVAVNRCLTLOPDRPSRELLKHP 666
DB 309 ALFPHIGTKSNPPIPEHLSAESKDFLKLQKQEPHLRHSASNLQHP 356

RESULT 5
S20117
protein kinase BCK1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
M/Alternate names: protein J0906; protein kinase SLK1; protein kinase SSP1; protein J01
C/Species: Saccharomyces cerevisiae
C/Date: 23-Apr-1993 #sequence_rev18-Nov-1994 #text_change 24-Sep-1999
C/Accession: S20117; S50298; S22285; S19061; JQ1432; S56872; S30794; JQ1118
R/Costigan, C.; Gehring, S.; Snyder, M.
Mol. Cell. Biol. 12, 1162-1178, 1992
A>Title: A synthetic lethal screen identifies SLK1, a novel protein kinase homolog impl
A/Reference number: S20117; MUID:92186847; PMID:1545797
A/Accession: S20117
A/Molecule type: DNA
A/Residues: 1-1478 <COS>
A/Cross-references: EMBL:M84389
A/Experimental source: strain S288C
R/Miotsa, T.; Boles, E.; Schaeff-Geretschlaeger, I.; Schmitt, S.; Zimmermann, F.K.
Yeast 10, 1481-1488, 1994
A>Title: Sequence and function analysis of a 9.74 kb fragment of Saccharomyces cerevisi
A/Reference number: S50295; MUID:9516706; PMID:7671867
A/Accession: S50298
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-1478 <MIO>
A/Cross-references: EMBL:X77923; NID:g640004; PIDN:CAA54896.1; PID:g640009
R/lee, K.S.; Levin, D.E.

Mol. Cell. Biol. 12, 172-182, 1992
A>Title: Dominant mutations in a gene encoding a putative protein kinase (BCK1) bypass t
A/Reference number: S22285; MUID:92107166; PMID:1729597
A/Accession: S22285
A/Molecule type: DNA
A/Residues: 1-58; 'I', 60-1478 <LEB>
A/Cross-references: EMBL:X60227
A/Experimental source: strain EG123
R/lee, K.S.; Levin, D.E.
Submitted to the EMBL Data Library, June 1991
A/Description: An extragenic suppressor of mutations in the S. cerevisiae protein kinase
A/Reference number: S19061
A/Accession: S19061
A/Molecule type: DNA
A/Residues: 1-58; 'I', 60-263; 'P', 265-278; 'I', 280-702; 'S', 707-708; 'RP', 714; 'VITMT', 715-79
A/Cross-references: EMBL:X60227; NID:g3414; PIDN:CAA42786.1; PID:g3415
A/Experimental source: strain EG123
R/Irie, K.; Araki, H.; Oshima, Y.
Gene 108, 139-144, 1991
A>Title: A new protein kinase, SSP1, modulating the SMP3 gene-product involved in plasm
A/Reference number: JQ1432; MUID:92104496; PMID:1840547
A/Accession: JQ1432
A/Molecule type: DNA
A/Residues: 149-1478 <IRI>
A/Cross-references: EMBL:D10389; DDBJ:D90446
R/Miotsa, T.; Schaeff-Geretschlaeger, I.; Baur, A.; Boles, E.; Chalatzis, N.; Fournie
submitted to the Protein Sequence Database, September 1995
A/Reference number: S56855
A/Accession: S56855
A/Molecule type: DNA
A/Residues: 1-1478 <MIW>
A/Cross-references: EMBL:249370; NID:g1008269; PIDN:CAA83389.1; PID:g1008270; MIPS:YJL095
R/Chick, M.E.
submitted to the EMBL Data Library, March 1992
A/Reference number: S27437
A/Accession: S30794
A/Molecule type: DNA
A/Residues: 602-959; 'R', 961; 'R', 963-1085; 'V', 1087; 'SILIAHT', 1092-1094; 'RMD', 1101; 'TV', 11
A/Cross-references: EMBL:M88604; NID:g172073; PIDN:AAA21179.1; PID:g172074
C/genetics:
A/Genes: SGD:BCK1; SLK1; SSP1
A/Cross-references: SGD:S0003631; MIPS:YJL095W
C/Map position: 10L
C/Function:
A/Description: phosphotransferase; protein kinase; involved in cell proliferation
C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C/Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein ki
F:1173-1440/Domain: protein kinase ATP-binding motif
F:1181-1189/Region: protein kinase ATP-binding motif

Query Match: 16.6%; Score 574.5; DB 2; Length 1478;
Best Local Similarity 24.1%; Pred. No. 2.8e-16;
Matches 211; Conservative 122; Mismatches 270; Indels 271; Gaps 32;

QY 9 FSKLVLMNAGSGSTHTRRRRLMAIDAEVLAIEVQLQVEDVDQHSQSLQAVAPTSC 68
DB 620 FLKSLFLNTSGKIT-----IKDQKQO-----KKPAPLVS 653
QY 69 ENSSLHETVAREKTKGLSATRLSASSEDISDRLAGVSGVLPSTTTEQPKPA----- 121
DB 654 NNVPKLSVSKSMRSGTSS--LIASD-----VSLVTSSDITSPDEHAGSGRRY 704
QY 122 VOTGRPHSQCINASP-----LSHAQLMPAPASPCASAPVSDISKARPQAF 169
DB 705 PGTSPSYDYRVANTVTEELANWNIKEVLSHE-----NADKMYFKTSPKLEMLNPDKG 758
QY 170 VCKKPSAPQGRKSLQFOR-----NCEHRPDLQSPVFTGSRPP----- 213
DB 759 SKINPTPTTENESSKSFVYLAKDSTETIDPNHRESPTTKBELAPKAPAPPPANTSPQ 818
QY 214 -----SSNIHRPKPSRPV-----GSTSKLDATKSMTLDLGSASR-- 250
DB 819 RTLSTSKQKPKPIRVAVASTKISRKSKSKPLPQQLSSPIEASSSSSDSLTSSVTPASTHV 878

QY 251 -CDSPGCG3-----NSGNAVIPSDETVF---TP----- 275
 DB 879 LIPQPKANDVWRRLKTDQDSTSTPSLKMCKKVRNSSTVSTNSIFSPSPLLKRG 938
 QY 276 ----VEDKRLDVNTLNSIEPLLEASNP-----SSDTTFYKSEVAV--- 315
 DB 939 SKRVVSTSAADIFEE-----NDITPADAPMPEDSDSDSDSSDDIIMSKKKTAPETN 993
 QY 316 ----LSEKAKENDTVYDVVNHOKCKEKE-----AEESEALA 350
 DB 994 NENKDEKSDNSSTHDEIFYDSQTDQKERRKTFPPSPVYQNLKFFPPRLNDKPIIT 1053
 QY 351 IAMAMASQDAL-----PIVPOLOVE-----NGEDIIIIQODT 383
 DB 1054 EGIASPTSPKSLDLSLPKVVASRTEPTSPSRVPDPDSYEFIOGLNGKKNKPLNQAKT 1113
 QY 384 P-----ETLPGH-----TYAKQ---PYRED 400
 DB 1114 PKTKTIRTAHEASLARKNSVYLKRONTKMGTMRWEVTEENHMSINKAKNSKGEYKEF 1173
 QY 401 AEMLKGOQIGLAFSSCYAQDVGCTGTLMAVKQTVVRNNTSSQREY---VEALREIRN 457
 DB 1174 A-WMKGBEMIGKSGFSAVYICLVNTTGBMAVAKOV-VPKYSSONBAIISTVEALRSEVST 1231
 QY 458 MGLNHPNIIIMLGATCEKSNYNLFTEWAGSGSVAMHLSKYGAFKESVIVNTYEQLLRG 517
 DB 1232 LMDLDLNTVQYVGFENKNNTYSLFLEYVAGSGVSLIRMYGRFDEPLIHLITQYLKGL 1291
 QY 518 SYLHENQIIRHDYKANLLIDSTGQRLIADFGAARLASKGTGAGBFGQQLGTAFA 577
 DB 1292 AYHLSHGIIHRDMKANLLIDODG-ICKISDFGISRK--SKDIYSNS-DWTMKGTFMMA 1347
 QY 578 PEVLARKQO-YGRSCDVWSVCAIIEWAKAPMNAEKSHNLIRKIASATTAPISPH 636
 DB 1348 PEKVDTKQGISAKVDIWSJCTIVLEMPAGKRPWS---NEEVAMFKIGKSKSAPPIPD 1404
 QY 637 LSPGL-----RDVAVRCLLEQPDQPPSRRELLKHP 666
 DB 1405 TLPLISQIGRNPLDACFEINPEKRPANELLSHR 1438

RESULT 6

A39723

protein kinase byr2 (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe)

N.Alternate names: protein kinase ste8

C.Species: Schizosaccharomyces pombe

C.Date: 14-Feb-1992 #sequence, revision 14-Feb-1992 #text_change 15-Sep-2000

C.Accession: A39723; S30094; T39860; T40139

Mol. Cell. Biol. 11, 3554-3563, 1991

File: byr2, a Schizosaccharomyces pombe gene encoding a protein kinase capable of par

reference number: A39723; MUID:91260705; PMID:2046669

A.Accession: A39723

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-659 <WAN>

R.StyKarsdottir, U.; Egel, R.; Nielsen, O.

Mol. Gen. Genet. 235, 122-130, 1992

A.Title: Functional conservation between Schizosaccharomyces pombe ste8 and Saccharomyce

A.Reference number: S30094; MUID:93062799; PMID:1435723

A.Accession: S30094

A.Molecule type: DNA

A.Residues: 1-659 <STY>

A.Cross-references: EMBL:K68851; NID:g5106; PIDN:CA48731.1; PID:g5107

R.Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

submitted to the EMBL Data Library, August 1997

A.Reference number: T39860

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-659 <WOO>

A/Cross-references: EMBL:298270; PIN:CA10981.1; GSPDB:GN00067; SPDB:SPBC1D7.05C
 A/Experimental source: strain 972h-; cosmid CID7
 R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
 submitted to the EMBL Data Library, June 1997
 A/Reference number: Z21907
 A/Accession: T40139
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 298-659 <W02>
 A/Cross-references: EMBL:297211; PIN:CA10150.1; GSPDB:GN00067; SPDB:SPBC2F12.01
 A/Experimental source: strain 972h-; cosmid c2F12
 C/Genetics:
 A/Map position: 2
 C/Superfamily: protein kinase byr2; protein kinase homology; SAM homology
 C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F.1-66/Domain: SAM homology <SAM>
 F.1-66/Domain: protein kinase homology <KIN>
 F.400-408/Region: protein kinase ATP-binding motif

Query Match 16.4%; Score 568; DB 1; Length 659;

Best local similarity 26.9%; Pred. No. 2, 3e-16;

Matches 181; Conservative 112; Mismatches 267; Indels 112; Gaps 24;

QY 46 LGEVDTVDGHQ-----DSIQAVAPTSCLF-----NSLEHTYHREKTKGSLSATRLSAS 95
 DB 46 LGIENTAKKQKQLKQDYLREF-PPCILRFACNGQTRAVOSRGDYQTLLIALKFFSL 104
 QY 96 EDISRLAGVSGVLSSTTTEQPKPRAVQTKGRPHQCNSSPSLHQAQMFPAAPSCSA 155
 DB 105 EDASKRIVVSSSRKILTEEFKQI-----CFNSSPERDRLLIVPEKPC--- 152
 QY 156 PSVPDISKH-----RQAFVPCIKIPASQTORKFFSLQFORNSKRRDSQSLSP 204
 DB 153 PSFEDLRKWEIELQAPALSSQSSLSPLSSVLPSTQKREVR-----SNMAP 202
 QY 205 VFTQSRPP--SSNI-----HRPKSPRPVGSSTKLGDAATKSSNTLDLSASRCDSE 255
 DB 203 FESYGRPPSELINSRLSDFFPDHQPRLKTKTISNLRNLTIRTSQGNL----- 252
 QY 256 GGGNSGNAVITSDVETFPVPEDKRLDVNTLNSI--EDL--LEASMSSDTTFYKSE 312
 DB 253 ---GNFGQELIPRSSRRAPSELVCEP---SSLRISVADVRLPRIDRGPPPLTVSST 306
 QY 313 VAVLSPEKAKENDT-----YKDVVNHOKCKEKEAE-----EALAIAMAMAS-- 358
 DB 307 QRISRPPSLQKSTITWGVPEPLYQ--NGNEKSKTNVFSBSAHGNHQLVSFSPGSPRT 364
 QY 359 QDALPIVPOLOVNGEDIIIIQODTPELPGHTKAKOPYREDAEWLKGOQIGLAFSSCY 418
 DB 365 EQPSPISP--TSTSEDTWTLEEDTD-----QGIKWIRGALISGSGFGQY 409
 QY 419 QADQVGTGTLMAVKQVTV--VNTSSSEQVEVLEALREIRMGHNHPNIIIMLGATCK 476
 DB 410 LGNNASSGELMAVKQVITLDSVESKDRNAKLLDALGELTALLQELSHHTVYLSGNLS 469
 QY 477 SNYNLFTEWAGSGSVAMHLSKYGAFKESVIVNTYEQLLRGSLYHENOIIRHDYKANLL 536
 DB 470 DHNITFLEVPGSGVAGLITMGSGFEETIVKFIKOTLKGRLYLSRGIVNHDIKANIL 529
 QY 537 IDSTGQRLIADFGAARLA--SKGTAGEFOGQLLGTIAFAPEVLARQOYVGRSCDWS 594
 DB 530 VDNKG-KIKISDFGISKLELNSTSTKTGAPRFGSSFWMAPEVVKOTMTEKTDIWS 588
 QY 595 VGCATTEWAKAPMNAEKSHNLALIRKIASATTAPISPSLSEGLRVAARCLELQO 654
 DB 589 LGLCLVTEMLTSGPY--PNCQOMQAFRIGE-NILPEPNSISSALDFEKTAFIDCN 644
 QY 655 DRPPSRRELLKHP 666
 DB 645 LRPTASELLSHR 656

RESULT 7

A96662

hypothetical protein F24D7.11 [imported] - Arabidopsis thaliana

C/Specties: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C/Accession: A96662

R/Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzman, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

Reference number: A86141; MUID:21016719; PMID:11130712

Accession: A96662

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-883 <STO>

A/Cross-references: GB:A8005173; NID:g6456172; PIDN:AAF09160.1; GSPDB:GN00141

A/Gene: F24D7.11

A/Map position: 1

Query Match 15.5%; Score 536; DB 2; Length 883;
 Best Local Similarity 26.1%; Pred. No. 6.1e-15;
 Matches 173; Conservative 103; Mismatches 243; Indels 144; Gaps 25;

89 TRLSASSEDISDLGAVGVGLPSTTTEOPKPAVQTKGRPHSCGLNS-----SP 137
 57 SRPSSPSSTSTVSRQCSFAERSPAVPLPRPV---RHHVSTTSGMNGSORPGLDAN 112
 138 LSHAQMFAPAPAPCCSAPSVDPDISKRPQAFVPCPKIPASP----- 179
 113 LKSWPLPRKP---HGATSPDNTGAKPD-FATASVSSSSGVDIPSDLSPLASDCE 167
 180 ---QTKRPSLQQRNCSEHRSDQLSPVTSQRPSPSSNIHRP----- 220
 168 NGNRTPVNISSRQSMNSKMSAEMFKVPVKNRIILSASPRRPLGTHVKNLQIPORDLV 227
 221 -----KPSRP-----VPGSTSKLG-DATKSSMTLTLGASRCDSDFFGGGSGNA 264
 228 LGSAPDSLSPSRSPKRSFTPDQVSHGLISPKYSDVLSGQC-SFPGSGNSGN 286
 265 VIPSDD-ETVFTVEDKCRDLVNTLNSIEDLLEASMPSSDTTVTFKSEVAVLSP- 319
 287 SLGDMAVQLFWP-QSRG---SPECSPVSPRMTSPGSSRIQ---SGAVTFLHPRAG 338
 320 KAENDTYKDVVNHQCKEKMEABEEBALAIAMASADALPIYQLOVENGEDIIII 379
 339 STTGSPTRRIDDRQSGHR-----LPLRP-----LII 365
 380 QDQTPETLPHTKA-----KOPYREDA-----EWLKGQIGLGAFFSSCYAQDVGTG 427
 366 SNTCPSP-PTYSATSPSPSPRAEATVSPGSRMKKGLLGLGSGHGYLLGPNSSG 424
 428 LMAVKQTVYRNTSSSEOEVEALREIRMGHLMHNPILIRMLGATCEKSNYLFLEWMA 487
 425 MCMKVEVTLCSDDPKSRES-AQQLGGEISVLSRLRHQNIYQYGSERVDDKXLYEYVS 483
 488 GGSVAHLISRYGAFKESVINYTBQLRGLSYHENOIHRDYKGNALLDSTGQRLRIA 547
 484 GGSIVYKLOEYGGFGENAIVNYTQQLISGLAYHAKNTVHRDIKGANILVDPIHG-RVKVA 542
 548 DFGAARLAKGAGGAGFQGLGLTIFAMPEVLRGQYGR-SCDVWSVGCATIEEMCAK 606
 543 DFGAKKITTQ-SGPLSFK---GSPYMAPEVYKNSGNSLAVDINSGLCTVLEMAATK 597
 607 PPNNAEKSHNLALIFKIASATTAPSPSHLSPGLRDAVAVRCLQPODRPPSRRLKHP 666
 598 PPNNS---QYEGVAPAMFKIGNSKELPDIPLHSECKQFVTKCLQDRNPANPFTAQLDDHA 654

RESULT 8

S51380

protein kinase STE11 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)

N/Alternate names: protein L8039.10; protein YLR362W

C/Specties: Saccharomyces cerevisiae

C/Date: 23-Feb-1995 #sequence_revision 11-Aug-1995 #text_change 21-Jul-2000

C/Accession: S51380; A36456

R/Du, Z.

submitted to the EMBL Data Library, December 1994

A/Description: The sequence of S. cerevisiae cosmid 8039.

A/Reference number: S51377

A/Accession: S51380

A/Molecule type: DNA

A/Residues: 1-738 <DUZ>

A/Cross-references: EMBL:U9103; NID:g609404; PIDN:AAB67571.1; PID:g609414; GSPDB:GN0001;

R/Rhodes, N.; Connell, L.; Ertede, B.

Genes Dev. 4, 1862-1874, 1990

A/Title: STE11 is a protein kinase required for cell-type-specific transcription and sig

A/Reference number: A36456; MUID:91115076; PMID:2276621

A/Accession: A36456

A/Molecule type: DNA

A/Residues: 1-717 <RHO>

A/Cross-references: GB:X53431

C/Genetics:

A/Gene: SGD:STE11; MIPS:YLR362W

A/Cross-references: SGD:S0004354; MIPS:YLR362W

A/Map position: 12R

C/Superfamily: protein kinase byr2; protein kinase homology; SAM homology

C/Keywords: ATP; phosphotransferase; protein kinase

F:38-104/Domain: SAM homology <SAM>

F:34-733/Domain: protein kinase homology <KIN>

F:442-450/Region: protein kinase ATP-binding motif

Query Match 15.2%; Score 528.5; DB 1; Length 738;
 Best Local Similarity 26.5%; Pred. No. 1e-14;
 Matches 185; Conservative 104; Mismatches 214; Indels 195; Gaps 28;

26 RMRRLMATADVEIEMAVQLGVEDVVDGHQDSLQAV-----APTGLNLSLEHT----Y 77
 172 RLPHELLATNSNGEVKMWQDYDVFVLDYTKVNLHLVYELVTICHADRVKKNLIEV 231
 78 HREKT--GKGLSATR-----LSASSEDISDLGAVGVGLPSTTTEOPKPAVQTKGRPH 129
 232 SKQTPSDALISTSKULYRTLSALQ-----VG-PSSNL-----LAQNGIGH 275
 130 SGLNSPLSHQMLMPAPAPCCSAPSVDPDISKRPQAFVPCPKIPASPOTQKRSIQ 188
 276 NNAEGLRLIDNTE-----KDIRQLQFNQRPSEFISTNLGAYFPHTDMK---R 320
 189 PQNCSE-HRDSQSLSPVTSQSRPPSSNIHRKPRPVPGRSKLD-ATSSMTLDLG 246
 321 LQTKRESFRHSRLISA-----QRPLSABSNNTGDIILKHSNAVDMA 364
 247 SASRCDSDFGGSGNSGNAVYPSDETFTVEDEKCRDLVNTLNSIEDLLEASMPSSDTT 306
 365 LLOGLD-----QTRLSKL-----DTT 381
 307 VTFKSEVAIVSPKAEENDTYKDVVNHQCKEKMEABEEBALAIAMASADALPIYV 366
 382 ---KIPKLHAKRPDNDALIS-----NQLDELTVSGEIE-----DHDFF--- 417
 367 QLOVENGEIIIIQDQTPETLPHTKAKOPYREDAEWLGGQIGLGAFFSSCYAQDVGTG 426
 418 ---GSDSDV-----SLP-TKIATP-----KMWLKGACIGSGSPGVYIGMAHYTG 459
 427 TLMAVKQTVYRNT-----SSOE-----VV 448

Db 460 ELMAVQVEIKNNICVPTDNNKANSDENNEOEQEKIEDVGAIVSHPTKNTNHRKV 519
QY 449 EALREIRMMGHNLHNPNIIRMLGATCEKSNYNLFIEEMAGSVAAHLISKYGAPEKSVIN 508
Db 520 DALQHMMLLKEHNNITYYTYGASOEGGNLNFLEVPQGSVSNLNNYGPREEBLIN 579
QY 509 YREBQIRGLSYLHENQIHRDVKGANLLIDSTGQRLIADFGAARLAKGTGAGEPQO 568
Db 580 FTROILIGVAYLHKNNIHRDIDIGANILIDIKG-CVKITDFGISKPLSKPLNKKONK-RAS 637
QY 569 LGTIAFMAPEVLRGOQYGRSCDWSVGCALIEMACAKPPMNAEKSHNLALFLIASAT 628
Db 638 LQSGFVWMSPEVVKQYATTAKADISTGCVVIEFPGKHP---PPSQWQALFKIGINT 694
QY 629 TAPSIPLSHLSPGLRDVAVRCLQLQPODRPPRELLKHP 666
Db 695 T-PEIRSMATSEKGNFLRKAFLDQYRPSALELLQHP 731

RESULT 9

T30565
MAP kinase kinase kinase - Yeast (Kluyveromyces marxianus var. lactis)
C:Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
Accession: T30565
Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
J. Mol. Biol. 288, 337-352, 1999
Kobayashi, J. J.; Kitchin, L.; Gengenbacher, U.; Heinsch, J. J.
A:Title: Characterization of KLBCL1, encoding a MAP kinase kinase kinase of Kluyveromyces
A:Reference number: Z20862; PMID:99262846; PMID:10329146
A:Accession: T30565
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1338 <JAC>
A:Cross-references: EMBL:AJ005079; NID:g3021328; PID:CA06336.1; PID:g3021329
C:Genetics:
A:Note: BCK1
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 15.1%; Score 525; DB 2; Length 1338;
Best Local Similarity 27.3%; Pred. No. 2, 5e-14;
Matches 182; Conservative 123; Mismatches 267; Indels 95; Gaps 25;

QY 64 PISCLN---SLEHTVHRKTKGKGL-----SATRLSASS---EDISD-R 101
Db 676 PAAAKNVSESPLESPKLDKNGKTIYQKPKRPPPLTERSSRSVSLSGQDINLVK 735
QY 102 LAGVSVGLSSSTTEQPKP---AVQTKGRPHSGCLNSSPLSHQMLFPAPSAFCSSAPSV 158
Db 736 ESPVQSTFPASTQVWVPQYKALETL-KPKRS-----SADLSIRPMW 777
QY 159 PDISKHPQAFVPCIKPSASPTQRFKSLQ-----FORNCSEHSDQLSPV-- 205
Db 778 SLRQPERSSSLNKLKTLSTKRLNTKNGKPLVTSSTADIPENISFADAEISDSD 837
QY 206 FTQSRPPSSNIHRPKPSRPVPGSTSKLDGATKSSMTLDSGASRCDDSPFGGSGNSG-- 263
Db 838 YGASSDEIIMSDRKISINDVPEFSPNTED-----TIDLVTGDTTQVSGATEGSDTPK 891
QY 264 --AVIPSDSTVTPVVDKRLDVTNELNSIEDLEASMPSSSTTYTPKSEVAVLSPEKA 321
Db 892 KVALRSPDPVYVQNLK-KFPDADLD-NPLLEGLTPPSPNADSPSPRPFKSLKTS 949
QY 322 ENDDTYKDVNNHOK-----CKEKMAEEEBALAIAMASADALPIVQ-LQVEN---- 372
Db 950 EQQPAPLSRGSSQPLTVYKSLKPKRTKIRI-IAQASSEAKRNEVQKQKRTTKW 1008
QY 373 GEDIIIIQDPTPLFGHTKAKQPYREDAEWLKGQOIGLAFSSCYQAQDVGITLMAVK 432
Db 1009 GKQVAVITDKRTISIKSRNSREYKFA-WIKGEIIGKSGFCAVYVLTALVTTGEMLVK 1067
QY 433 QYTYVRNTSSEQ---EVEALREIRMMGHNLHNPNIIRMLGATCEKSNYNLFIEEMAGG 489
Db 1068 QVT-VPEFSSODESAISWEALKSEVSTLKDNLHNVIVQYLGEFKNGIYSFLLEVAGG 1126

QY 490 SYAHLISKYGAPEKSVINYTEQLRLGLSYLHENQIHRDVKGANLLIDSTGQRLIADP 549
Db 1127 SVGSLIRMYGRDDQILRLHTQVLEGLAYLSKGLHRDMKADULLDNDV-CRISDF 1185
QY 550 GAARLAKGTGAGEPQOGLGTIAFMAPEVL-RGOQYRSCDWSVGCALIEMACAKPP 608
Db 1186 GISRKSNNTYSN---DMTRGTVMMAPEWDTAHGSAKVYDLSLGCVLIEFPGKRP 1242
QY 609 WNAEKSHNLALIFKIASATPAISPSH-----LSPGLRDVAVRCLQLQPODRPPRELLK 664
Db 1243 WS---NFEVVAAMFQIGSKTAPPIPDQTKDVSFAGSGFLDQCFEIDPEKFTADSLVG 1299
QY 665 HPEVFTT 671
Db 1300 HPECKTS 1306

RESULT 10

G96575
probable MEK kinase MAP3Ka, 84794-81452 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96575
R:Theologis, A.; Eckert, J. R.; Palm, C. J.; Federspiel, N. A.; Kaul, S.; White, O.; Alonso, C.; Chiu, C. W.; Chung, M. K.; Corn, L.; Conway, A. B.; Conway, A. R.; Creasy, T. H.; Dewar, K.; Jensen, N. F.; Hughes, B.; Hultzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J. L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C. A.; Li, J. H.; Li, Y. Y.; Lin, X.; Liu, S. X.; Liu, Z. A.; Lueros, J. S.; Malt, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzbeyer, S. L.; Schwartz, J. R.; Shinn, P.; Southwick, A. M.; Sun, H.; Tallon, I. Ker, M.; Wu, D.; Yu, G.; Frazer, C. M.; Venter, J. C.; Davis, R. W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A66141; PMID:21016719; PMID:11130712
A:Accession: G96575
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-608 <STO>
A:Cross-references: GB:AB005173; NID:g10645340; PID:AA021460.1; GSPDB:GN00141
C:Genetics:
A:Gene: P22G10.18
A:Map position: 1

Query Match 15.0%; Score 519.5; DB 2; Length 608;
Best Local Similarity 26.7%; Pred. No. 2e-14;
Matches 142; Conservative 86; Mismatches 190; Indels 113; Gaps 14;

QY 190 QNCSSEHSDQLSPVFTQSRPPSSNIHRPKPSRPVPGSTSKLDGATKSSMTLDSGS 249
Db 7 RSKCKNKQDNHR--GIISTRDRIKSSAVVDPPLTPTRGGT-----P 46
QY 250 RCDDSPFGGSGNNAVIPSEDT-----VTFPVDEKRLDVTNELNSIEDLEAS 299
Db 47 RCSRFP-AGASSAFSGFDSSTKKGHLPRPLSPVSIHHDHVSSTSVSSVS 105
QY 300 MPSSDT-----TYTFKSEVAVLSPEKAENDDTYKDVNNHOKCKEMAESEEA 348
Db 106 SSSADDQSLVSRGKGVKFNVAAPRSEKVS----- 139
QY 349 LAIAMASADALPIVQLQVENEDIIIIQDPT-----PETLPGHT 391
Db 140 -----PKATITTRPTSPRHQLSG--VYLSSTGRNDGRSSSECHLPPLPPTSP 192
QY 392 KAKQPYRED-----AEWLKGQOIGLAFSSCYQAQDVGITLMAVKQYTYVRNTS 441
Db 193 SAVHSRIGGQYETSPSGFTYKKGKPLGSGFTFGQYVIGFENKGMCAIKVXKYSDDQ 252
QY 442 SQCEVEALREIRMMGHNLHNPNIIRMLGATCEKSNYNLFIEEMAGSVAAHLISKYGA 501
Db 253 T-SKRCIQNLQINLNLQCHPNIVQYGGSLSEBTLISVLEYSGSGIHTLNDYSGF 311
QY 502 KESVIVNTEQLRLGLSYLHENQIHRDVKGANLLIDSTGQRLIADFGAARLAKSGTG 561

Db 312 TEVVIQNTTQIAGLAVLHGRNTVHRDIDGANTLVDPNGE-ITKADFGAKKVTAST- 369
 QY 562 AGEPQGLCTTAFMAPEVLRGQO-YGRSCDWSVGCALITEMACAKPPMAEKHSNHAL 620
 Db 370 ---MLSEFKSPYMAPEVMSQNGYTHAVDIWSLGTITLEMATSKPPMS---QFEGVAA 422
 QY 621 IFKIATATPAPSIPIHSLSPGLRDVAVRCLELOQDPDPRELLKHPVFRFT 671
 Db 423 IFKIGNSKOTPEIPDLHLSNDANKFIRLCQRPNTVPTASOLHEHPRLNT 473

RESULT 11

T38073
 speine/threonine-protein kinase mbk1 - fission yeast (Schizosaccharomyces pombe)
 Species: Schizosaccharomyces pombe
 Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 Accession: T38073
 R:Conor, R.; Church, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, April 1996
 A:Reference number: Z21767
 A:Accession: T38073
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1116 <CON>
 A:Cross-references: EMBL:Z70690; PIDN:CAA94620.1; GSPDB:GN00066; SPDB:SPAC1F3.02c
 A:Experimental source: strain 972h-; cosmid c1f3
 C:Genetics:
 A:Gene: pmk1; SPDB:SPAC1F3.02c
 A:Map position: 1

Query Match 14.4%; Score 499.5; DB 2; Length 1116;
 Best Local Similarity 24.5%; Pred. No. 2.3e-13;
 Matches 174; Conservative 119; Mismatches 293; Indels 123; Gaps 22;

QY 42 EVIQLGVETDHDQDLSIAVAFTSCLENGSLBHTVREKTKGL-SATRLSASEDISD 100
 Db 429 EITDAGPNLSLSGHPD-----NKTYGFSAPMLAVVPELPSR 467
 QY 101 RLAG-----VSVLPSSTTTEQPKPAVOTKGRPHSQCLNSPLSHAOLMPAPSA 150
 Db 468 RFQGFKEIRKAGKEMATKILDATEAGEKKKF-TVCRPHKKVTLKMPLENGSSAPQSPSS 526
 QY 151 PCSSASVDPISGHRQAPFPCIKPSASPTOKKFSLOFQPNCSHRDSQLSPVFTQSR 210
 Db 527 NTSASVLTFRFVNRD---PPPEPTETSLRKNTLT-RRPSIRHARS---SPYIDTGH 578
 QY 211 PPSSNIHRKPSRPVPGSTKLGDAATKSMTLDLGASRCDSFGGSGNSGNAVIPSDE 270
 Db 579 NEASKSTHSTFDPKASKSSNSLKESEVETALSEIPFEDAPALDES-DLSGDPFMAIQPKOS 637
 QY 271 TVETPVED---KCRDLVNTELNSSLIEDLLEAMSPS-----DTVTTF-----KS 311
 Db 638 SSGVPEKNHNHNIQSKLSINTEAATDLK-ANELSSPKTPEYCRGDDRSISLSPYLRKS 696
 QY 312 EVAVLSPEKAE-----NDPTKQD-----DVFNQCKEKEA 343
 Db 697 KHIREPPSSKVINSGNWEVRPSADLYEDVDRFPFRYDLKVLVVDQSHWSPSPKVS 756
 QY 344 EEEBALAIAAMASODALPIVPOLOVEN-----GEDIIIIOQDPETLLPGH 390
 Db 757 RPKMKSVRLAKRASEKKEIRHARANKSGNLRNSSTLWMSRIYELKPDPTTITSGSV 816
 QY 391 TKAKOPYREDAEWLKQOQIGLGAFFSSCYQADVGTGTLMAVKQVTVYRNTSS---QEE 446
 Db 817 VSGNATFK---WMKGLINGTYGKVFLLAMNINTGELIIVKQVEIRPQTINGRHQDLRKD 872
 QY 447 VVALAEETIRMGHILHNPNIIRMLGATCEKSNNTLPIEMAGGSVAHLISKYAFKESV 506
 Db 873 IVDSINAEISMDLHNLIVQYLFKEKTTDSTIFLEYVSGSIGRCILNNYSPFEQVL 932
 QY 507 INTTEQLRGLSYLHENQIHRVVKGANLIDSTGCLRIADFGAARLASKGTGAGEFQ 566

Db 933 RFVSRQVLVGLSYLHSGKIIHRDLKADNLLIDPDGV-CRISDFGSKH--SDNVYNDAN 989
 QY 567 GQLGTTAFMAPEVLG--QQYGRSCDWSVGCALITEMACAKPPMAEKHSNHALIFKI 624
 Db 990 LSKQGSIFWMAPEVHNDHOGYSKADVWSLGCVVELEMAGRBPWSTDE---AIOAMFKL 1046
 QY 625 ASATATPAPSIPIHSLSPGLRDVAVR-----CLELOQDPDPRELLKHPVFR 669
 Db 1047 GTEKKAPEIPSELVSOVSPALQIPLNACFTVNDVPRPTAEELNHPMK 1095

RESULT 12

H86221
 hypothetical protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: H86221
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pedersen, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Jensen, N.F.; Hughes, B.; Hutzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MOID:21016719; PMID:11130712
 A:Accession: H86221
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-652 <STO>
 A:Cross-references: GB:AE005172; NID:92342692; PIDN:AAB70419.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 13.8%; Score 479; DB 2; Length 652;
 Best Local Similarity 37.0%; Pred. No. 9.1e-13;
 Matches 112; Conservative 51; Mismatches 90; Indels 50; Gaps 10;

QY 388 PGHTKAKOPYREDAEWLKQOQIGLGAFFSSCYQADVGTGTLMAVKQVTVYRNTSSQEEV 447
 Db 57 PANTVMAPE---PISRKQGLIRGAFGYTMGMNLSGELLAVKVLIAANAS--KEK 111
 QY 448 VVALREIRMGHILHNPNI-----RMUGA-----TCEKSN-----YMLFIEWMA 487
 Db 112 TQLEEEVKKLKLKLSHNPVIVSNQWYCLLNAYGFNTSLCYLSNVSREDDTLNILEFVP 171
 QY 488 GGSVALLSKYGAFKESVYVINTYEQLLRGLSYLHENQIHRVVKGANLIDSTGQRLTA 547
 Db 172 GGSISLLEKFGFPSPSVARTYRQLLLGLEYLHNAIMHRDIKANIIVDNKG-CIKLA 230
 QY 548 DFGAARLASKGAGEFGQGLGTTAFMAPEVL--RGOQYG-----587
 Db 231 DFGASQVAFELAMTG--AKSMKGTIPYMAPEVILDTGHSFPDDLCPILISHKPAIYL 288
 QY 588 RSCDWSVGCALITEMACAKPPMAEKHSNHALIFKIATATPAPSIPIHSLSPGLRDVAVR 647
 Db 289 SSADIVSVCVTIVMTGKAPMS--QOYKEVAIFIGTKSHPIPIPTLSSADKFLK 346
 QY 648 CLE 650
 Db 347 CLQ 349

RESULT 13

T51625
 MAPK alpha protein kinase (EC 2.7.1.-) [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 08-Sep-2000
 C:Accession: T51625
 R:Jouanin, S.; Hamal, A.; Lepoint, A.S.; Tregear, J.W.; Kreis, M.; Henry, Y.
 Gene 229, 171-81, 1999

A:Title: Characterisation of novel plant genes encoding MEKK/STELL and RAF-related proteins
 A:Reference number: Z24447; MID:9916996; PMID:10095117
 A:Accession: T51625
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-582 <OU>
 A:Cross-references: EMBL:AJ010090; PID:CAA08994.1
 C:Genetics:
 A:Gene: MAP3K alpha
 C:Keywords: phosphotransferase

Query Match 13.6%; Score 472.5; DB 2; Length 582;
 Best Local Similarity 26.6%; Pred. No. 1.5e-12;
 Matches 130; Conservative 72; Mismatches 162; Indels 125; Gaps 12;

238 KSMITD-----LGSASRCDSPFGGSGNNAVISDER-----VFPVVDCKR 281
 DB KSAVAVDPPLTPRTGGTPRCRREF-AGASSAFSGFSDTEKKGHPPLRPPLSPVSIHQ 86
 QY 282 LDVTELENSIEDLEASMPSSDT-----TVTFKEVAVALSPKAEKNDTYKDD 330
 DB 87 DHVSGSTSGTSVSSVSSSGSADDSQIVASRGKGVKNVAAPRSPERSV----- 138
 QY 331 VVHNOCKEKMEAEBEALAIAMASASDAPLPIVQLOVENCEDITITIQDT----- 383
 DB 139 -----PKAATITTRPTSPRHORLSG--VVSLESTGRNDGR 173
 QY 384 -----PETLPGHTAKOPYRED-----AEMLKGOQIGLAFSCYQADY 423
 DB 174 SSSSECHPLRPPTSPSPSAVHSGRIGGGYETSPSGSTWKKKFTGGTFCGVYGFNS 233
 QY 424 GTGTLAAVQTVYVNTSSSEOEVEALREIRMGHLNHNPIRMIGATCEKSNYNLF 483
 DB 234 EKGKCAIKVKVITSDQT-SKECLKQNGEINLNLQCPNIVQYYSLESETLSVYL 292
 QY 484 EMMAGGSVAHLISKYGAFFESVINTTEQLRGLSTLHENQIHRDVKGANLLIDSTGR 543
 DB 293 EYVSGGSIHKLKDYGSFTEPVIQNTROTLAGIAYHGRNIVHRIKGNILFK----- 347
 QY 544 LMIADGAARLASKGTGGEFGQLLGTAFMAPEVLRGQ-QYGRSCDVMSGCALIE 602
 DB 348 -----GSPYMAPEVMSQNGYTHAVDWSJGCTILEN 380
 QY 603 ACAKPPMAEKSHNLALIFKIASATTAPSIPEHLSPGLDVAVRCLELOPDRPSREY 662
 DB 381 AISKPPMS---QREGVAALFKIGNSKOTPEIPHLISNDANFRLCQNRPTVRPTASQ 437
 QY 663 LKHVPFRFT 671
 DB 438 LEHPLRLNT 446

LT 14
 33
 serine/threonine-specific protein kinase ARA.KIN (EC 2.7.1.-) - Arabidopsis thaliana
 N:Alternate names: protein T15F16.5
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Sep-1999
 C:Accession: T01833; S65789
 R:Antonou, B.; Le, T.
 submitted to the EMBL Data Library, August 1998
 A:Description: The sequence of A. thaliana T15F16.
 A:Reference number: Z14443
 A:Accession: T01833
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-608 <NT>
 A:Cross-references: EMBL:AF076275; NID:93293582; PID:AC28196.1; PID:93377823
 A:Experimental source: cultivar Columbia
 R:Covic, L.; Lew, R.R.
 Biochim. Biophys. Acta 1305, 125-129, 1996
 A:Title: Arabidopsis thaliana cDNA isolated by functional complementation shows homology
 A:Reference number: S65789; MID:96180314; PMID:8597596

A:Accession: S65789
 A:Molecule type: mRNA
 A:Residues: 'YVRE', 119-236, 'LDPLLIGDRLG', 248-338, 'V', 340-358, 'G', 360-369, 'EVALKRPYNEEG'
 A:Cross-references: EMBL:L43125; NID:9871811; PID:AAA99196.1; PID:9871812
 C:Genetics:
 A:Map position: 4
 A:Antons: 353/2; 381/3; 402/3; 455/2; 479/3; 499/3; 537/3
 A:Note: T15F16.5
 C:Superfamily: unaassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:331-587/Domain: protein kinase homology <KIN>
 F:339-347/Region: protein kinase ATP-binding motif

Query Match 13.3%; Score 462; DB 2; Length 608;
 Best Local Similarity 24.6%; Pred. No. 4.1e-12;
 Matches 166; Conservative 94; Mismatches 258; Indels 156; Gaps 22;

54 GHQSLQAVAPTSCLNSLEHTVREKTKGLSATRLSASSEDISDRLAGSVGLPST 113
 DB 13 GRGDDKNTTPVRRLEERRDAARNIVD-----AASCSSSAEDLS----- 52
 QY 114 TTEQKPAVOTGRDHSQCLNSPLSHAQMPAPSA-----PCSSAPSPVD 160
 DB 53 -----VTSLSMTRELPEPEPTFRIGGVGEMDRIVSLGSGSD 93
 QY 161 ISKHPQAFVPCIKPSAPQTKRFSLOFORNCSEHRSDQSPVFTQSRPPSSNIHRP 220
 DB 94 DLATFDAAEACKKSSSPDVNRFKSFIDLK-----VRDQD-----LSRE 133
 QY 221 KSRPVPGSTSLGDAKTSMTLDLGSASRCDSPGCG-----GNSGNVVISDETVPFP 275
 DB 134 GSGGVVSGDS---MNRKVQGDUSEAGP---SGGLVTELSERGNLTPVDRLVADG 184
 QY 276 VEDCKR-----LDVTELENSIEDL-----LEASM 300
 DB 185 VVENRRVWERTPTIYKSKYLVNPNVAVGVGGIKGLRPPVLPKPPAMRPPIDHG 244
 QY 301 PSSDTTVTFKSEVAVLSPKAEKNDTYKDVHNOCKEKMEAEBEALAIAMASASD 360
 DB 245 SSMDFLTHPAPSEIVRFPSSSSSS--EDGCBEERKEBEAEAEAGAFIOLGDTADBT 302
 QY 361 ALPIVQLOVENCEDITITIQDTPETLPGHTAKOPYRDAMKLGQOIGLAFSCYQA 420
 DB 303 C-----SFTTNGDSSSTVSNTPYPOGAIL-----TSWQGLQIGKSPGSLVHG 350
 QY 421 QVGTGTLAAVQTVYVNTSSSEOEVEALREIRMGHLNHNPIRMIGATCEKSNYN 480
 DB 351 IS-GGDDPFAVKEVSL--DQSQAOECIQOLEGELKLSQLQHOINVRYRGTAKGSNLY 408
 QY 481 LFIEMAGGSVAHLISKYGAFFESVINTTEQLRGLSTLHENQIHRDVKGANLLIDST 540
 DB 409 IFLELVYQSLKLKYQRY-QLRDSVSVLYTRQILDLKYLHKGFIHRDIKCANILVDAN 467
 QY 541 GQRLRIADFGAARLASKGTGGEFG--QLLGTAFMAPEVLRGQ---YGRSCDVMSV 595
 DB 468 G-AVKLADPGLK-----VSKFNIDIKSCGTPPMAPEVINRSDGYSPLIWSL 518
 QY 596 GCALIEMACKPPMAEKSHNLALIFKIASATTAPSIPEHLSPGLDVAVRCLELOP 655
 DB 519 GCTVLEMTGQIPYS---DLEFVQALFRIGR-TLPEVDTISLDAKRLILKCLKVNPBE 574
 QY 656 RPPSRELLKHVPFR 669
 DB 575 RPTAELNLNHPFR 588

RESULT 15
 T03022
 MAP kinase kinase kinase - human
 C:Species: Homo sapiens (man)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 05-Nov-1999
 C:Accession: T03022
 R:Takekawa, M.; Posas, F.; Salto, H.

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